Serial No. 09/864,954 Filed: May 24, 2001

Amendments to the Claims:

- 1. (Currently amended) A process for determining whether or not a test sample originating from or containing human <u>mammary</u> cells has a tumor progression potential, wherein a second sample originating from non-tumor cells from the same individual or a different individual of the same species is also used, which process comprises the following steps:
 - (a) incubating said samples under stringent hybridization conditions with a nucleic acid probe which is selected from the group consisting of:
 - (i) a nucleic acid consisting of SEQ ID NO:1;
 - (ii) a nucleic acid with a sequence which is complementary to <u>SEQ ID</u>

 NO:1-any nucleic acid of (i); and
 - (iii) a nucleic acid which, though not identical to the nucleic acids of (i) and (ii), due to the degeneracy of the genetic code encode a polypeptide having the amino acid sequence of the polypeptide encoded by SEQ ID NO:1; and with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and
 - (iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and
 - (b) determining the approximate amount of hybridization of each respective sample with said probe; and
 - (c) comparing the approximate amount of hybridization of the test sample to an approximate amount of hybridization of said second sample to identify whether or not the test sample contains a lower amount of the nucleic acid than does said second sample, wherein when the amount of hybridization of said test sample is greater than the amount of hybridization

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of said second sample, said test sample contains cells having which may have a tumor progression potential.

- 2. (Currently amended) A process for determining whether or not a test sample originating from or containing human <u>mammary</u> cells has a tumor progression potential, which process comprises the following steps:
 - (a) incubating a first compartment of said sample under stringent hybridization conditions with a first nucleic acid probe which is selected from the group consisting of:
 - (i) a nucleic acid consisting of SEQ ID NO:1;
 - (ii) a nucleic acid with a sequence which is complementary to <u>SEQ ID</u>

 NO:1any nucleic acid of (i); and
 - (iii) a nucleic acid which, though not identical to the nucleic acids of (i) and (ii), due to the degeneracy of the genetic code encode a polypeptide having the amino acid sequence of the polypeptide encoded by SEQ ID NO:1; and with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and
 - (iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and
 - (b) incubating a second compartment of said sample under stringent hybridization conditions with a second nucleic acid probe being a housekeeping gene;
 - (c) determining the approximate amount of hybridization of said samples with said first and second probe;
 - (d) identifying whether or not the test sample contains an at least 3-fold amount of nucleic acid hybridizing with the first probe in comparison to the amount of

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nucleic acid hybridizing with the second probe, wherein when said test sample contains a <u>3-fold greater</u> amount of hybridization with the first nucleic acid probe than with the second nucleic acid probe, said test sample contains cells <u>having-which may have</u> a tumor progression potential.